B1 "The invention was made with the support of federal funding from NIH grant R01 HL55362."

On page 32, please replace the third paragraph (beginning with "In one preferred embodiment") of the originally-filed application with the following paragraph:

"In one preferred embodiment, the isolated polynucleotide comprises a nucleotide sequence encoding the polypeptide comprising SEQ ID NO: 2. Importantly, in contrast to the published sequence of Langmann et al. which codes for a protein of 2201 amino acids based on a predicted start methionine found in exon 3 (Langmann et al., *Biochem. Biophys. Res. Comm.*, 257: 29-33 (1999) (GenBank Accession No. AJO12376), the presently claimed nucleotide sequence contains 50 exons and codes for a protein of 2261 amino acids (see Figure 4). The corresponding nucleotide sequence of the present invention contains a coding sequence that includes an additional 180 nucleotides at the 5' end corresponding to the following 60 amino-terminal amino acids: MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKA (SEQ ID NO. 58). Given that there is an in-frame stop codon 6 to 9 nucleotides upstream from this location, the newly predicted start site is the first methionine codon that could produce a continuous open reading frame. Alignment of this new ABC1 cDNA sequence with related ABC transporter sequences ABCR and ABC-C (also known as ABC3) which also contain open reading frames for"

B2

On page 36, please replace the third paragraph (beginning with "In another embodiment") of the originally-filed application with the following paragraph:

"In another embodiment, the isolated polynucleotide comprises the 3' flanking region of ABC1. Several 3' untranslated regions have been identified which may represent alternate sites of polyadenylation of the ABC1 transcript. Preferably, the 3' flanking region contains regulatory sequences. For example, the full length 3' UTR (SEQ ID NO: 6) contains 46 sequences (AA)nCU/UC(AA)n (SEQ ID NO: 59) which have been shown to be necessary for binding of

B3

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Vigilin. Vigilin, a ubiquitous protein with 14K homology domains, is the estrogen-inducible vitellogenin mRNA 3'-untranslated region binding protein (*J. Biol. Chem.*, 272: 12249-12252 (1997)). In addition to binding HDL, Vigilin has been shown to bind to the 3' flanking region of mRNAs and to increase the half-life of the mRNA transcript (*Mol. Cell. Biol,* 18:3991-4003 (1998)). Thus, the 3' flanking region could be altered, for example, to increase the binding of Vigilin, thereby increasing the half-life of the ABC1 mRNA. Preferably, the isolated polynucleotide comprises"

On page 58, please replace the second paragraph (beginning with "The dosage regimen") of the originally-filed application with the following paragraph:

"The dosage regimen for treating a cardiovascular disease with a composition comprising an ABC1 polynucleotide or ABC1 expression vector is based on a variety of factors, including the type of cardiovascular disease, the age, weight, sex, medical condition of the patient, the severity of the condition, the route of administration, and the particular compound employed. Thus, the dosage regimen may vary widely, but can be determined routinely using standard methods. For example, the amount of ABC1 polynucleotide or ABC1 expression vector to be administered is an amount sufficient to increase cholesterol efflux from the cells of a mammalian subject. Such amount can be determined, for example, by measuring the plasma HDL-cholesterol level of a subject before and after administration of the ABC1 polynucleotide or ABC1 expression vector. A sufficient amount of ABC1 polynucleotide or ABC1 expression vector is an amount that increases the plasma HDL-cholesterol level of a subject. Accordingly, the clinician can titer the dosage and modify the route of administration to obtain the optimal therapeutic effect. A typical dosage may range from about 0.1 g/kg to about 100 mg/kg or more, depending on the factors mentioned above."

On page 76, please replace the first paragraph (beginning with "against a synthetic") of the originally-filed application with the following paragraph:

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"against a synthetic peptide corresponding to KNQTVVDAVLTSFLQDEKVKES (SEQ ID NO. 60) located at the C-terminus, as described in Example 11. The anti-ABC1 antibodies can be detected using several methods known in the art, including, for example, western blotting, immunoprecipitation, and FACS, wherein the detection can be accomplished using radioactive, colorometric, or fluorescent labeling. One preferred method for measuring the amount of ABC1 protein in a cell sample is immunoprecipitation, wherein biotinylated ABC1 proteins are contacted with anti-ABC1 antibody and the bound anti-ABC1 antibody is detected using streptavidin horse radish peroxidase."

B5

On page 101, please replace the fourth paragraph (beginning with "To determine which") of the originally-filed application with the following paragraph:

"To determine which portion of the 5' flanking region of ABC1 retains transcriptional activity in response to nuclear ligands, various plasmids containing a different portion of the 5' flanking region and a luciferase reporter gene were transfected into RAW 264.7 cells treated with at least one ligand for the nuclear receptors. Using this system, an sterol response element corresponding to nucleotides 1480-1510 of SEQ ID NO: 3 was identified. The sterol response element contains a direct repeat-4 element TGACCGatagTAACCT (SEQ ID NO: 61). Confirmation of the sterol response element was obtained using site-directed mutagenesis and band-shift assay techniques."

B6

On page 102, please replace the third paragraph (beginning with "Site-Directed Mutagenesis") of the originally-filed application with the following paragraph:

B7

"Site-Directed Mutagenesis: The sterol response element corresponding to nucleotides 1480-1510 of SEQ ID NO: 3 was mutated in the 1080-1643 sequence described above using site-directed mutagenesis. Specifically, the response element containing a direct repeat-4 element

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